



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 144217

TO: Nita M Minnifield
Location: rem/3c01/3c18
Art Unit: 1645
Tuesday, February 22, 2005
Case Serial Number: 10/680349

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Minnifield,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527

STIC-Biotech/ChemLib

144217

my

From: Minnifield, Nita
Sent: Thursday, February 03, 2005 11:04 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

10/680349

STIC

Please do a commercial and interference sequence search on SEQ ID NO: 41 (nt) and SEQ ID NO: 42 (aa) of this application.

Please provide a paper copy of the results.

Thanks,
Minnifield,
~~71796~~
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

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Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: 2/2 _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using sw model

Run on: February 17, 2005, 16:48:20 ; Search time 40 Seconds
(without alignments)
673.517 Million cell updates/sec

Title: US-10-680-349-42

Perfect score: 1462
Sequence: 1 MNVKKILVNSALISLMSILP.....ASVTLVDVGFGEIGNRKFTF 280

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	629.5	43.1	276	2 JE0218	28k surface antigen
2	620	42.4	286	2 JE0219	28k surface antigen
3	603	41.2	280	2 JE0217	28k surface antigen
4	583	39.9	278	2 JE0216	28k surface antigen
5	565	38.6	284	2 I40882	major antigenic pr
6	515.5	35.3	287	2 JE0220	28k surface antigen
7	386.5	26.4	282	2 I39648	major surface prot
8	227.5	15.6	133	2 JE0221	28k surface antigen
9	119.5	8.2	264	2 I54668	heat resistant agg
10	107.5	7.4	239	2 AH0541	probable outer mem
11	104.5	7.1	738	2 S01892	hemolysin A precu
12	102	7.0	1176	2 A27826	DNA-directed RNA p
13	101.5	6.9	415	2 B70448	3-oxoacyl-l-acyl-ca
14	100	6.8	1582	2 AC1153	adhesin homolog lm
15	98	6.7	3890	2 C89921	hypothetical prote
16	97.5	6.7	274	2 AC395	heat resistant agg
17	97.5	6.7	1174	2 S28876	DNA-directed RNA p
18	97.5	6.7	1271	2 A45555	glutamate rich pro
19	97.5	6.7	1310	2 AD1380	glycosidase homolo
20	95	6.5	1004	2 B25039	outer cell wall pr
21	95	6.5	1578	2 AD1512	peptidoglycan boun
22	94.5	6.5	474	2 F97264	endo-beta-N-acetyl
23	93.5	6.4	558	2 E95111	endo-beta-N-acetyl
24	93	6.4	180	2 H71639	hypothetical prote
25	93	6.4	608	2 H64473	hypothetical prote
26	93	6.4	745	2 T51370	hypothetical prote
27	92.5	6.3	219	2 AF2658	conserved hypotet
28	92.5	6.3	219	2 C97440	hypothetical prote
29	92.5	6.3	401	2 F86754	prophage p12 prote

30	92.5	6.3	585	2 C69336	probable electron
31	91.5	6.3	721	2 C97980	endo-beta-N-acetyl
32	91.5	6.3	1234	2 A25884	DNA-directed RNA p
33	91.5	6.3	1635	2 A10452	hemolysin (impor
34	91	6.2	282	2 S16617	opacity protein op
35	91	6.2	588	2 AG0517	penicillin-binding
36	91	6.2	1348	2 B23496	TYB protein - year
37	91	6.2	1598	2 S69667	TYB protein - year
38	91	6.2	1770	2 S69653	TYB protein - year
39	91	6.2	1770	2 S58651	TYB protein - year
40	91	6.2	1770	2 S70233	TYB protein - year
41	91	6.2	1770	2 S69666	TYB protein - year
42	91	6.2	1770	2 S69650	TYB protein - year
43	91	6.2	1770	2 S70230	TYB protein - year
44	91	6.2	1771	2 S53592	TYB protein - year
45	91	6.2	1810	2 S69973	TYB protein - year

ALIGNMENTS

```

RESULT 1
JE0218
28k surface antigen 5 - Ehrlichia chaffeensis
N/Alternate names: MAPI
C/Species: Ehrlichia chaffeensis
C/Accession: JE0218
R/Reddy, G.R.; Sultana, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A/Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe
A/Reference number: JE0216; MUID:98321180; PMID:9647746
A/Accession: JE0218
A/Molecule type: DNA
A/Residues: 1-276 <RED>
A/Cross-references: UNIPROT:Q93DD2; UNIPROT:Q9AC19; GB:AF062761

Query Match      43.1%; Score 629.5; DB 2; Length 276;
Best local Similarity 47.9%; Pred. No. 8.3e-44;
Matches 137; Conservative 41; Mismatches 87; Indels 21; Gaps 6;

QY 1 MNVKKILVNSALISLMSILPYQSPADPVGSRNDNKEGYISAKYNPSISHRKSABERT 60
DB 1 MNVKKVFIKRSALISLISLPVGSFSDPAGSGINGN---FYISGKMPASHGVPSAKX- 56
QY 61 PLNGNSLTKKVFGLKQGD-----ITKDDPTVAKPIDQNNLISGFSGISYMDG 114
DB 57 ---ERNTTVGVGFLKQWWDGSAISNSPNDVFTVSNTSPKYEKNPFLGAFAGISMDG 112
QY 115 PRILEEAAVQCFNPKNQDNDNDNGEYVYKHFSKRDME---DOQYVVLKNDGITFMS 170
DB 113 PRILEEVESEYETDVANQGN--YKREARVYCHLSNSAADSASANNFPLKNGILDLS 170
QY 171 LMVNTCYDITAGVSVFVYACAGIGADITIFKDLNLKFAVQKIGISYPIPEVSAPFG 230
DB 171 FMLNACVYVGEIGIFPSFYICAGICTDLVSMFEATNPKISYQKGLGSLYSISPEASVFIG 230
QY 221 GYHHVITGNKPEKIVITPVLANDPQ--TTASAVTLVDVGFGEIG 275
DB 221 GHFRVITGNBFRDIPITIPGSLTLAGKNYPAIVLIDVCHFGIEWG 276

RESULT 2
JE0219
28k surface antigen 2 - Ehrlichia chaffeensis
N/Alternate names: MAPI
C/Species: Ehrlichia chaffeensis
C/Accession: JE0219
R/Reddy, G.R.; Sultana, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A/Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe
A/Reference number: JE0216; MUID:98321180; PMID:9647746

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OM protein - protein search, using sw model

Run on: February 17, 2005, 16:44:35 / Search time 166 Seconds
(without alignments)
652.367 Million cell updates/sec

Title: US-10-680-349-42

Perfect score: 1462

Sequence: 1 MWYKILVRSALISILP.....ASVTLDVGFGEIGMRETF 280

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_1dDec04:*
1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003s:*
7: geneeqp2003bs:*
8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1462	100.0	280	AAU96116	AAU96116 Ehrlichia
2	1462	100.0	280	ABG77938	ABG77938 Ehrlichia
3	1462	100.0	280	ADA09781	ADA09781 E. canis
4	1202.5	82.3	283	AAU06944	AAU06944 E. chaffe
5	1202.5	82.3	283	AAU96106	AAU96106 Ehrlichia
6	1202.5	82.3	283	AAU73413	AAU73413 Ehrlichia
7	1202.5	82.3	283	ABG77936	ABG77936 Ehrlichia
8	1202.5	82.3	283	ADA09737	ADA09737 E. chaffe
9	715	48.9	165	AAU06970	AAU06970 E. canis
10	644.5	44.1	281	AAU06943	AAU06943 E. chaffe
11	644.5	44.1	281	AAU96105	AAU96105 Ehrlichia
12	644.5	44.1	281	AAU73418	AAU73418 Ehrlichia
13	644.5	44.1	281	ABG77935	ABG77935 Ehrlichia
14	642.5	43.1	281	ADA09735	ADA09735 E. chaffe
15	629.5	43.1	276	AAU51095	AAU51095 Ehrlichia
16	629.5	43.1	276	AAU36189	AAU36189 Ehrlichia
17	629.5	43.1	276	AAU04199	AAU04199 Variable
18	622	42.5	286	AAU51092	AAU51092 Ehrlichia
19	621	42.5	288	AAU06959	AAU06959 E. canis
20	621	42.5	288	ABG77950	ABG77950 Ehrlichia
21	621	42.5	288	ADA09765	ADA09765 E. canis
22	620	42.4	286	AAU06946	AAU06946 E. chaffe
23	620	42.4	286	AAU36186	AAU36186 Ehrlichia
24	620	42.4	286	AAU04196	AAU04196 Variable
25	620	42.4	286	AAU96108	AAU96108 Ehrlichia

26	620	42.4	286	AAU73415	AAU73415 Ehrlichia
27	620	42.4	286	ABG77938	ABG77938 Ehrlichia
28	620	42.4	286	ADA09741	ADA09741 E. chaffe
29	606	41.5	280	ABG77953	ABG77953 Ehrlichia
30	605	41.4	280	AAU06948	AAU06948 E. chaffe
31	605	41.4	280	AAU96110	AAU96110 Ehrlichia
32	605	41.4	280	ABG77940	ABG77940 Ehrlichia
33	605	41.4	280	ADA09745	ADA09745 E. chaffe
34	603	41.2	280	AAU51094	AAU51094 Ehrlichia
35	603	41.2	280	AAU36188	AAU36188 Ehrlichia
36	603	41.2	280	AAU04198	AAU04198 Variable
37	603	41.2	280	AAU73417	AAU73417 Ehrlichia
38	601	41.1	280	AAU06962	AAU06962 E. canis
39	601	41.1	280	AAU71479	AAU71479 Ehrlichia
40	601	41.1	280	AAU96102	AAU96102 Ehrlichia
41	601	41.1	280	ADA09771	ADA09771 E. canis
42	592	40.5	285	AAU06957	AAU06957 E. chaffe
43	592	40.5	285	AAU73408	AAU73408 Ehrlichia
44	592	40.5	285	ABG77949	ABG77949 Ehrlichia
45	588	40.2	278	AAU71477	AAU71477 Ehrlichia

ALIGNMENTS

1-3

RESULT 1
AAU96116
ID AAU96116 standard; protein; 280 AA.

XX AAU96116;

DT 02-JUL-2002 (first entry)

XX Ehrlichia canis p28-2.

KW Ehrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial.

OS Ehrlichia canis.

PN W0200222782-A2.

PD 21-MAR-2002.

XX 12-SEP-2001; 2001WO-US028759.

XX 12-SEP-2000; 2000US-00660587.

XX (RERE-) RES DEV FOUND.

XX Walker DH, Yu X, McBride JW;

PI WPI; 2002-351882/38.

DR N-PSDB; ABR68876.

PT New recombinant homologous 28 kilodalton immunodominant protein from

XX Ehrlichia canis, useful for treating Ehrlichia canis infections.

PS Claim 16; Fig 14; 106pp; English.

XX The invention relates to a recombinant homologous 28 kDa immunodominant

CC protein, p28, (I), of Ehrlichia canis. (I'), a 28-kDa antigen preferably

CC dispersed in a pharmaceutically acceptable carrier, is useful for

CC inhibiting E. canis infection in a subject. (I) is useful in the

CC development of vaccines and serodiagnostic that are particularly

CC effective for disease prevention and serodiagnosis. AAU96100-AAU96118

CC represent the 28-kDa antigen amino acid sequences of the invention

XX SQ Sequence 280 AA;

Query Match 100.0%; Score 1462; DB 5; Length 280;

Best Local Similarity 100.0%; Pred. No. 1.9e-138; Mismatches 0; Indels 0; Gaps 0;

Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using SW model

Run on: February 17, 2005, 16:49:10 ; Search time 43 Seconds
(without alignments)
486.087 Million cell updates/sec

Title: US-10-680-349-42

Perfect score: 1462

Sequence: 1 MNXKILVRSALISLMSILP.....ASVTLDVGYFGGIGMRFTF 280

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents, AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfltest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1462	100.0	280	3	US-09-660-587-42
2	1462	100.0	280	4	US-09-314-701-46
3	1462	100.0	280	4	US-09-811-007A-42
4	1202.5	82.3	283	3	US-09-660-587-10
5	1202.5	82.3	283	4	US-09-261-358A-10
6	1202.5	82.3	283	4	US-09-201-458-6
7	1202.5	82.3	283	4	US-09-314-701-4
8	1202.5	82.3	283	4	US-09-811-007A-10
9	644.5	44.1	281	3	US-09-660-587-9
10	644.5	44.1	281	4	US-09-261-358A-9
11	644.5	44.1	281	4	US-09-201-458-5
12	644.5	44.1	281	4	US-09-811-007A-9
13	644.5	43.9	281	4	US-09-314-701-2
14	629.5	43.1	276	3	US-08-953-326-18
15	629.5	43.1	276	4	US-09-553-662-18
16	629.5	43.1	276	4	US-10-062-994-18
17	621	42.5	288	4	US-09-314-701-32
18	620	42.4	286	3	US-08-953-326-15
19	620	42.4	286	3	US-09-660-587-12
20	620	42.4	286	4	US-09-261-358A-12
21	620	42.4	286	4	US-09-201-458-8
22	620	42.4	286	4	US-09-314-701-8
23	620	42.4	286	4	US-09-553-662-15
24	620	42.4	286	4	US-10-062-994-15
25	620	42.4	286	4	US-09-811-007A-12
26	605	41.4	280	3	US-09-660-587-14
27	605	41.4	280	4	US-09-261-358A-14

28	605	41.4	280	4	US-09-201-458-10	Sequence 10, Appl
29	605	41.4	280	4	US-09-314-701-12	Sequence 12, Appl
30	605	41.4	280	4	US-09-811-007A-14	Sequence 14, Appl
31	603	41.2	280	3	US-08-953-326-17	Sequence 17, Appl
32	603	41.2	280	4	US-09-553-662-17	Sequence 17, Appl
33	603	41.2	280	4	US-10-062-994-17	Sequence 17, Appl
34	601	41.1	280	3	US-09-660-587-6	Sequence 6, Appl
35	601	41.1	280	4	US-09-261-358A-6	Sequence 6, Appl
36	601	41.1	280	4	US-09-314-701-38	Sequence 38, Appl
37	601	41.1	280	4	US-09-811-007A-6	Sequence 6, Appl
38	588	40.2	278	4	US-09-660-587-2	Sequence 2, Appl
39	588	40.2	278	4	US-09-261-358A-2	Sequence 2, Appl
40	588	40.2	278	4	US-09-201-458-2	Sequence 2, Appl
41	588	40.2	278	4	US-09-811-007A-2	Sequence 2, Appl
42	588	40.2	307	4	US-09-314-701-36	Sequence 36, Appl
43	587	40.2	285	4	US-09-314-701-30	Sequence 30, Appl
44	583	39.9	278	3	US-08-953-326-16	Sequence 16, Appl
45	583	39.9	278	3	US-09-660-587-13	Sequence 13, Appl

ALIGNMENTS

```
RESULT 1
US-09-660-587-42
Sequence 42, Application US/09660587
Patent No. 6392023
GENERAL INFORMATION:
APPLICANT: Walker, David H.
APPLICANT: McBride, Jere W.
APPLICANT: Yu, Xue-De
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
FILE REFERENCE: D6152CIP2
CURRENT APPLICATION NUMBER: US/09/660,587
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 09/261,358
PRIOR FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 42
LENGTH: 280
TYPE: PRT
ORGANISM: Ehrlichia canis
FEATURES:
OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-09-660-587-42

Query Match      100.0%; Score 1462; DB 3; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.2e-151;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNXKILVRSALISLMSILPYOSPADPVGSRITDNKGFYSIAKYNPSISHPRKSAET 60
    |||
DB 1 MNXKILVRSALISLMSILPYOSPADPVGSRITDNKGFYSIAKYNPSISHPRKSAET 60
    |||

QY 61 PINGNSLTKKVFGLKKGDIITKKDFTRYAPGIDFONNLISGSGSIGSMQPRIELE 120
    |||
DB 61 PINGNSLTKKVFGLKKGDIITKKDFTRYAPGIDFONNLISGSGSIGSMQPRIELE 120
    |||

QY 121 AAYQFPKNTDNDTNGEYTHYHFAISRDAMEDQYVVLKNDGITFMSLMVNTCYDIT 180
    |||
DB 121 AAYQFPKNTDNDTNGEYTHYHFAISRDAMEDQYVVLKNDGITFMSLMVNTCYDIT 180
    |||

QY 121 AAYQFPKNTDNDTNGEYTHYHFAISRDAMEDQYVVLKNDGITFMSLMVNTCYDIT 180
    |||
DB 121 AAYQFPKNTDNDTNGEYTHYHFAISRDAMEDQYVVLKNDGITFMSLMVNTCYDIT 180
    |||

QY 181 AEGVSFVPYACAGIGADLITFMDLNKFAVOGKIGISYPIETBVSAFIGYHGVGNK 240
    |||
DB 181 AEGVSFVPYACAGIGADLITFMDLNKFAVOGKIGISYPIETBVSAFIGYHGVGNK 240
    |||

QY 241 FEKIPVITPVVNDAPQTSASVTLVDVGYFGGIGMRFTF 280
    |||
DB 241 FEKIPVITPVVNDAPQTSASVTLVDVGYFGGIGMRFTF 280
    |||

RESULT 2
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OM protein - protein search, using sw model

Run on: February 17, 2005, 16:57:26, Search time 133 Seconds

(without alignments)
688.929 Million cell updates/sec

Title: US-10-680-349-42

Perfect score: 1462

Sequence: 1 MYKKILVRSALISLMSILP.....ASVTLDVGFGEIGMRFPT 280

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1462	100.0	280	US-09-811-007-42	Sequence 42, Appl
2	1462	100.0	280	US-10-062-924-42	Sequence 42, Appl
3	1462	100.0	280	US-10-059-964-48	Sequence 48, Appl
4	1462	100.0	280	US-10-062-051-42	Sequence 42, Appl
5	1462	100.0	280	US-10-062-920-42	Sequence 42, Appl
6	1462	100.0	280	US-10-314-639-48	Sequence 48, Appl
7	1462	100.0	280	US-10-680-349-42	Sequence 42, Appl
8	1262.5	82.3	283	US-09-846-808-14	Sequence 14, Appl
9	1202.5	82.3	283	US-09-811-007-10	Sequence 10, Appl
10	1202.5	82.3	283	US-10-062-624-10	Sequence 10, Appl
11	1202.5	82.3	283	US-10-059-964-4	Sequence 10, Appl
12	1202.5	82.3	283	US-10-062-051-10	Sequence 10, Appl
13	1202.5	82.3	283	US-10-284-986-14	Sequence 14, Appl

14	1202.5	82.3	283	US-10-062-920-10	Sequence 10, Appl
15	1202.5	82.3	283	US-10-314-639-4	Sequence 4, Appl
16	1202.5	82.3	283	US-10-369-293-14	Sequence 14, Appl
17	1202.5	82.3	283	US-10-285-042-14	Sequence 14, Appl
18	1202.5	82.3	283	US-10-680-349-10	Sequence 10, Appl
19	644.5	44.1	281	US-09-846-808-19	Sequence 19, Appl
20	644.5	44.1	281	US-09-811-007-9	Sequence 9, Appl
21	644.5	44.1	281	US-10-062-624-9	Sequence 9, Appl
22	644.5	44.1	281	US-10-062-051-9	Sequence 9, Appl
23	644.5	44.1	281	US-10-284-986-19	Sequence 19, Appl
24	644.5	44.1	281	US-10-062-920-9	Sequence 9, Appl
25	644.5	44.1	281	US-10-369-293-19	Sequence 19, Appl
26	644.5	44.1	281	US-10-285-042-19	Sequence 19, Appl
27	644.5	44.1	281	US-10-680-349-9	Sequence 9, Appl
28	644.5	43.9	281	US-10-059-964-2	Sequence 2, Appl
29	644.5	43.9	281	US-10-314-639-2	Sequence 2, Appl
30	629.5	43.1	276	US-10-062-994-18	Sequence 18, Appl
31	629.5	43.1	276	US-10-062-994-18	Sequence 18, Appl
32	629.5	43.1	276	US-10-722-077-18	Sequence 18, Appl
33	621	42.5	288	US-10-059-964-32	Sequence 32, Appl
34	621	42.5	288	US-10-314-639-32	Sequence 32, Appl
35	620	42.4	286	US-09-846-808-16	Sequence 16, Appl
36	620	42.4	286	US-09-811-007-12	Sequence 12, Appl
37	620	42.4	286	US-10-062-994-15	Sequence 15, Appl
38	620	42.4	286	US-10-062-624-12	Sequence 12, Appl
39	620	42.4	286	US-10-059-964-8	Sequence 8, Appl
40	620	42.4	286	US-10-062-994-15	Sequence 15, Appl
41	620	42.4	286	US-10-062-051-12	Sequence 12, Appl
42	620	42.4	286	US-10-284-986-16	Sequence 16, Appl
43	620	42.4	286	US-10-062-920-12	Sequence 12, Appl
44	620	42.4	286	US-10-314-639-8	Sequence 8, Appl
45	620	42.4	286	US-10-369-293-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-811-007-42
Sequence 42, Application US/09811007
Publication No. US20030185849A1
GENERAL INFORMATION:
APPLICANT: Walker, David H.
APPLICANT: McBride, Jere W.
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
FILE REFERENCE: D6152CIP2
CURRENT APPLICATION NUMBER: US/09/811,007
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/660,587
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 42
LENGTH: 280
TYPE: PRT
ORGANISM: Ehrlichia canis
FEATURE:
OTHER INFORMATION: amino acid sequence of E. canis p28-2 protein
US-09-811-007-42

Query Match 100.0%; Score 1462; DB 10; Length 280;
Best Local Similarity 100.0%; Pred. No. 7,3e-136;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYKKILVRSALISLMSILPYOSFADPVGSRITNDKEGFYSKYNPISHPFKFSAEET 60
DB 1 MYKKILVRSALISLMSILPYOSFADPVGSRITNDKEGFYSKYNPISHPFKFSAEET 60
QY 61 PINGTSLTKVVGGLKKDDITKDDFTVAPRIDPQNNLISGSSGIGYMDGPRLELR 120
DB 61 PINGTSLTKVVGGLKKDDITKDDFTVAPRIDPQNNLISGSSGIGYMDGPRLELR 120

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OM protein - protein search, using sw model

Run on: February 17, 2005, 16:47:35 ; Search time 178 Seconds

(without alignments)
805.518 Million cell updates/sec

Title: US-10-680-349-42

Perfect score: 1462
Sequence: 1 NMVKILVRSALISIMSLIP.....ASVTLGVGFGGIGNRFT 280

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: uniprot_spport:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1462	100.0	280	Q9F476	Q9F476 ehrlichia c
2	1452	99.3	280	Q84HU1	Q84HU1 ehrlichia c
3	1224.5	83.8	283	Q8G8D6	Q8G8D6 ehrlichia c
4	1217.5	83.3	283	Q8G8I2	Q8G8I2 ehrlichia c
5	1217.5	83.3	283	Q8G8U4	Q8G8U4 ehrlichia c
6	1202.5	82.3	283	Q85358	Q85358 ehrlichia c
7	1124	76.9	282	Q9R443	Q9R443 cowdria rum
8	1120	76.6	282	Q9RW41	Q9RW41 cowdria rum
9	983	67.2	250	Q8VTT7	Q8VTT7 cowdria rum
10	665.5	45.5	275	Q93DD4	Q93DD4 ehrlichia c
11	655	44.8	276	Q8GCU0	Q8GCU0 ehrlichia c
12	651	44.5	276	Q85817	Q85817 ehrlichia c
13	648	44.3	280	Q9ZG09	Q9ZG09 ehrlichia c
14	647	44.3	276	Q93DD1	Q93DD1 ehrlichia c
15	645.5	44.2	281	Q93DD2	Q93DD2 ehrlichia c
16	644.5	44.1	281	Q9AC19	Q9AC19 ehrlichia c
17	644	44.0	280	Q85816	Q85816 ehrlichia c
18	628	43.0	280	Q93DD3	Q93DD3 ehrlichia c
19	621	42.5	288	Q9ZG02	Q9ZG02 ehrlichia c
20	620	42.4	286	Q52105	Q52105 ehrlichia c
21	605	41.4	280	Q52107	Q52107 ehrlichia c
22	605	41.4	291	Q8G8P3	Q8G8P3 ehrlichia c
23	601	41.1	280	Q9ADV3	Q9ADV3 ehrlichia c
24	600	41.0	280	Q9F473	Q9F473 ehrlichia c
25	599	41.0	291	Q8G921	Q8G921 ehrlichia c
26	598	40.9	291	Q8G602	Q8G602 ehrlichia c
27	592	40.5	285	Q916Y5	Q916Y5 ehrlichia c
28	589	40.3	287	Q8GCU3	Q8GCU3 ehrlichia c
29	588	40.2	278	Q9R3J3	Q9R3J3 ehrlichia c
30	588	40.2	278	Q9R8A5	Q9R8A5 ehrlichia c
31	588	40.2	278	Q9R8A6	Q9R8A6 ehrlichia c

ALIGNMENTS

32	588	40.2	278	2	Q9R8A7	Q9R8A7 ehrlichia c
33	588	40.2	278	2	Q9R8A8	Q9R8A8 ehrlichia c
34	588	40.2	278	2	Q9R8A9	Q9R8A9 ehrlichia c
35	588	40.2	307	2	Q9ZGJ1	Q9ZGJ1 ehrlichia c
36	583.5	39.9	277	2	Q8G8W7	Q8G8W7 ehrlichia c
37	583.5	39.9	277	2	Q8GCU1	Q8GCU1 ehrlichia c
38	583	39.9	278	2	Q52106	Q52106 ehrlichia c
39	583	39.9	278	2	Q9F472	Q9F472 ehrlichia c
40	573.5	39.2	279	2	Q8G8Q1	Q8G8Q1 ehrlichia c
41	573	39.2	278	2	Q8G8O5	Q8G8O5 ehrlichia c
42	569	38.9	280	2	Q8G8J3	Q8G8J3 ehrlichia c
43	567.5	38.8	281	2	Q9G6H1	Q9G6H1 cowdria rum
44	567	38.8	290	2	Q4G333	Q4G333 cowdria rum
45	566.5	38.7	271	2	Q69197	Q69197 ehrlichia c

AC	Q9F476	PRELIMINARY;	PRT;	280 AA.
DT	01-MAR-2001 (TREMREL. 16, Created)			
DT	01-MAR-2001 (TREMREL. 16, Last sequence update)			
DT	05-JUL-2004 (TREMREL. 27, Last annotation update)			
DE	P28-2 (Major outer membrane protein P30-10).			
GN	Name=p28-2; Synonyms=p30-10;			
OS	Ehrlichia canis.			
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;			
OC	Anaplasmataceae; Ehrlichia.			
OX	NCBI_TaxID=944;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Jake;			
RX	MEDLINE=99242757; PubMed=10225842;			
RA	McBride J.W., Yu X.J., Walker D.H.;			
RT	"Molecular cloning of the gene for a conserved major immunoreactive			
RT	28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic			
RT	antigen.";			
RL	Clin. Diagn. Lab. Immunol. 6:392-399(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Jake;			
RX	MEDLINE=20332107; PubMed=10974556; DOI=10.1016/S0378-1119(00)00256-0;			
RA	McBride J.W., Yu X.J., Walker D.H.;			
RT	"A conserved, transcriptionally active p28 multigene locus of			
RT	Ehrlichia canis.";			
RL	Gene 254:245-252(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Oklahoma;			
RX	MEDLINE=98371112; PubMed=9705412;			
RA	Ohashi N., Unver A., Zhi N., Rikhsa Y.;			
RT	"Cloning and characterization of multigenes encoding the			
RT	immunodominant 30-kilodalton major outer membrane proteins of			
RT	Ehrlichia canis and application of the recombinant protein for			
RT	serodiagnosis.";			
RL	J. Clin. Microbiol. 36:2671-2680(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Oklahoma;			
RX	MEDLINE=2153566; PubMed=1254561;			
RA	DOI=10.1128/IAI.69.4.2083-2091.2001;			
RT	Ohashi N., Rikhsa Y., Unver A.;			
RT	"Analysis of transcriptionally active gene clusters of major outer			
RT	membrane protein multigene family in Ehrlichia canis and E.			
RT	chaffeensis.";			
RL	Infect. Immun. 69:2083-2091(2001).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Arizona, California, New Mexico, and Venezuela;			
RX	MEDLINE=22461952; PubMed=12574308;			

1	840	100.0	840	10	US-09-811-007-41	Sequence 41, Appl1
2	840	100.0	840	13	US-10-062-524-41	Sequence 41, Appl1
3	840	100.0	840	14	US-10-062-051-41	Sequence 41, Appl1
4	840	100.0	840	14	US-10-062-920-41	Sequence 41, Appl1
5	840	100.0	840	18	US-10-680-349-41	Sequence 41, Appl1
6	840	100.0	840	18	US-10-731-554-41	Sequence 41, Appl1
7	840	100.0	843	13	US-10-059-864-47	Sequence 47, Appl1
8	840	100.0	843	15	US-10-314-539-47	Sequence 47, Appl1
9	840	100.0	843	18	US-10-901-714-47	Sequence 47, Appl1
10	840	100.0	843	18	US-10-901-774-47	Sequence 47, Appl1
11	598.6	71.3	852	13	US-10-059-864-3	Sequence 3, Appl1

12	598.6	71.3	852	15	US-10-114-639-3	Sequence 3, Appl 1
13	598.6	71.3	852	18	US-10-901-774-3	Sequence 3, Appl 1
14	598.6	71.3	852	18	US-10-901-774-3	Sequence 3, Appl 1
15	238.4	28.4	924	13	US-10-059-964-35	Sequence 35, Appl
16	238.4	28.4	924	15	US-10-114-639-35	Sequence 35, Appl
17	238.4	28.4	924	18	US-10-901-774-35	Sequence 35, Appl
18	238.4	28.4	924	18	US-10-901-774-35	Sequence 35, Appl
19	238.4	28.4	1607	10	US-09-811-007-1	Sequence 1, Appl 1
20	238.4	28.4	1607	13	US-10-062-662-1	Sequence 1, Appl 1
21	238.4	28.4	1607	14	US-10-062-051-1	Sequence 1, Appl 1
22	238.4	28.4	1607	14	US-10-062-920-1	Sequence 1, Appl 1
23	238.4	28.4	1607	18	US-10-680-349-1	Sequence 1, Appl 1
24	238.4	28.4	1607	18	US-10-731-554-1	Sequence 1, Appl 1
25	234	27.9	840	10	US-09-811-007-5	Sequence 5, Appl 1
26	234	27.9	840	13	US-10-062-662-5	Sequence 5, Appl 1
27	234	27.9	840	14	US-10-062-051-5	Sequence 5, Appl 1
28	234	27.9	840	14	US-10-062-920-5	Sequence 5, Appl 1
29	234	27.9	840	18	US-10-680-349-5	Sequence 5, Appl 1
30	234	27.9	840	18	US-10-731-554-5	Sequence 5, Appl 1
31	234	27.9	846	18	US-10-901-774-1	Sequence 1, Appl 1
32	234	27.9	846	18	US-10-901-774-1	Sequence 1, Appl 1
33	232.4	27.7	843	13	US-10-059-964-37	Sequence 37, Appl
34	232.4	27.7	843	15	US-10-114-639-37	Sequence 37, Appl
35	232.4	27.7	843	18	US-10-901-774-37	Sequence 37, Appl
36	232.4	27.7	843	18	US-10-901-774-37	Sequence 37, Appl
37	232.4	27.7	846	13	US-10-059-964-1	Sequence 1, Appl 1
38	232.4	27.7	846	15	US-10-314-639-1	Sequence 1, Appl 1
39	228.6	27.2	830	13	US-10-062-994-11	Sequence 11, Appl
40	228.6	27.2	830	13	US-10-062-994-11	Sequence 11, Appl
41	228.6	27.2	830	18	US-10-722-077-11	Sequence 11, Appl
42	217.4	25.9	867	13	US-10-059-964-31	Sequence 31, Appl
43	217.4	25.9	867	15	US-10-314-639-31	Sequence 31, Appl
44	217.4	25.9	867	18	US-10-901-774-31	Sequence 31, Appl
45	217.4	25.9	867	18	US-10-901-774-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

```

Sequence 41, Application US/09811007
Publication No. US20030185649A1
GENERAL INFORMATION:
APPLICANT: Walker, David H.
APPLICANT: McBride, Jere W.
APPLICANT: Yu, Xue-Jie
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Escherichia canis and Uses Thereof
FILE REFERENCE: D6152CIP2
CURRENT APPLICATION NUMBER: US/09/811,007
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/660,587
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 41
LENGTH: 840
TYPE: DNA
ORGANISM: Escherichia canis
FEATURES:
OTHER INFORMATION: nucleic acid sequence of E. canis p28-2
US-09-811-007-41

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Query Match	100.0%;	Score 840;	DB 10;	Length 840;
Best Local Similarity	100.0%;	Pred. No. 5.5e-172;		
Matches 840;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 1 ATGAATTAAGAAAATCTGTAGAAAGCGGTTAACTCAATAAAGTCAATCTTACCA 60

Db 1 ATGAATTAAGAAAATCTGTAGAAAGCGGTTAACTCAATAAAGTCAATCTTACCA 60

QY 61 TATCACTTTTGCAGATCTGTAGTTCAGAACTAATGATTAAGAAAGCTTTCAC 120

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OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 15:10:13 ; Search time 589 Seconds

(without alignment)
8442.415 Million cell updates/sec

Title: US-10-680-349-41

Perfect score: 840

Sequence: 1 atgaattacagaataatctt.....ttcgaatgaggttcaccttc 840

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn19808:*
2: geneseqn19908:*
3: geneseqn20008:*
4: geneseqn20018:*
5: geneseqn20028:*
6: geneseqn20038:*
7: geneseqn20048:*
8: geneseqn20058:*
9: geneseqn20068:*
10: geneseqn20078:*
11: geneseqn20088:*
12: geneseqn20098:*
13: geneseqn20108:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	840	100.0	840	6	ABK68876
2	840	100.0	843	6	ABK68876
3	840	100.0	843	6	ABK68876
4	600.2	71.5	852	2	AAK34744
5	600.2	71.5	852	2	AAK34744
6	598.6	71.3	852	9	ADA09736
7	450.8	29.0	849	6	AAK34770
8	243.4	28.4	924	2	AAK34761
9	238.4	28.4	924	2	AAK34761
10	238.4	28.4	924	6	ABK68876
11	238.4	28.4	924	6	ABK68876
12	238.4	28.4	1607	3	ABK68876
13	238.4	28.4	1607	3	ABK68876
14	238.4	28.4	1607	3	ABK68876
15	234	27.9	840	6	ABK68876
16	234	27.9	840	6	ABK68876
17	234	27.9	840	6	ABK68876
18	234	27.9	840	6	ABK68876
19	232.4	27.7	843	2	AAK34762
20	232.4	27.7	843	6	ABK68876

21	232.4	27.7	843	9	ADA09770	ADA09770 E. canis
22	232.4	27.7	846	2	AAK34743	AAK34743 DNA encod
23	232.4	27.7	846	9	ADA09734	ADA09734 E. chaffe
24	228.6	27.2	830	3	AAK68706	AAK68706 Ehrlichia
25	228.6	27.2	4683	3	AAV07179	AAV07179 Ehrlichia
26	228.6	27.2	4683	3	AAK68716	AAK68716 Ehrlichia
27	228.6	27.2	4683	4	AAK07578	AAK07578 DNA encod
28	217.4	25.9	867	2	AAK34759	AAK34759 DNA encod
29	217.4	25.9	867	6	ABK63291	ABK63291 DNA encod
30	217.4	25.9	867	6	ADA09764	ADA09764 E. canis
31	212.8	25.3	861	2	AAK34746	AAK34746 DNA encod
32	212.8	25.3	861	3	AAK68703	AAK68703 Ehrlichia
33	212.8	25.3	861	6	ABK63279	ABK63279 DNA encod
34	212.8	25.3	861	6	ADA09740	ADA09740 E. chaffe
35	210.4	25.0	756	6	ABK63307	ABK63307 Ehrlichia
36	208.8	24.9	756	6	AAK34742	AAK34742 DNA encod
37	207.2	24.7	843	2	AAK34748	AAK34748 DNA encod
38	207.2	24.7	843	3	AAK68705	AAK68705 Ehrlichia
39	207.2	24.7	843	6	ABK63281	ABK63281 DNA encod
40	207.2	24.7	843	9	ADA09744	ADA09744 E. chaffe
41	205	24.4	837	2	AAK34747	AAK34747 DNA encod
42	205	24.4	837	3	AAK68704	AAK68704 Ehrlichia
43	205	24.4	837	6	ABK63280	ABK63280 DNA encod
44	205	24.4	837	9	ADA09742	ADA09742 E. chaffe
45	203.8	24.3	842	2	AAV07177	AAV07177 Ehrlichia

ALIGNMENTS

RESULT 1	ABK68876	standard; DNA; 840 BP.
ID	ABK68876	
XX	ABK68876	
AC	ABK68876	
XX	ABK68876	
DT	02-JUL-2002	(first entry)
XX	02-JUL-2002	
DE	DNA encoding Ehrlichia canis p28-2.	
XX	DNA encoding Ehrlichia canis p28-2.	
KW	Ehrlichia canis infection; vaccine; serodiagnostic; gene; p28; ss;	
XX	antibacterial.	
OS	Ehrlichia canis.	
XX	Ehrlichia canis.	
PN	WO20022782-A2.	
XX	WO20022782-A2.	
PD	21-MAR-2002.	
XX	21-MAR-2002.	
PF	12-SEP-2001; 2001WO-US028759.	
XX	12-SEP-2001; 2001WO-US028759.	
PR	12-SEP-2000; 2000US-00660587.	
XX	12-SEP-2000; 2000US-00660587.	
PA	(RERE-) RES DEV FOUND.	
XX	(RERE-) RES DEV FOUND.	
PI	Walker DH, Yu X, McBride JW;	
XX	Walker DH, Yu X, McBride JW;	
DR	WPI; 2002-351882/38.	
XX	WPI; 2002-351882/38.	
PT	P-PSDB; AAU96116.	
XX	P-PSDB; AAU96116.	
PT	New recombinant homologous 28 kilodalton immunodominant protein from	
XX	Ehrlichia canis, useful for treating Ehrlichia canis infections.	
PS	Claim 5; Fig 14; 106pp; English.	
XX	Claim 5; Fig 14; 106pp; English.	
CC	The invention relates to a recombinant homologous 28 kDa immunodominant	
CC	protein, p28 (I) of Ehrlichia canis. (I), a 28-kDa antigen preferably	
CC	dispersed in a pharmaceutically acceptable carrier, is useful for	
CC	inhibiting E. canis infection in a subject. (I) is useful in the	
CC	development of vaccines and serodiagnostic that are particularly	
CC	effective for disease prevention and serodiagnosis. ABK68876-ABK68878	
CC	represent the 28-kDa antigen coding sequences and PCR primers of the	
CC	invention	

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OM nucleic - nucleic search, using BW model

Run on: February 19, 2005, 18:42:08 / Search time 194 Seconds
(without alignments)
7084.910 Million cell updates/sec

Title: US-10-680-349-41

Perfect score: 840
Sequence: 1 atgaattataagaataatctc.....ctggaatgaggtccaccttc 840

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	840	100.0	840	US-09-660-587-41	Sequence 41, Appl
2	840	100.0	840	US-09-811-007A-41	Sequence 41, Appl
3	840	100.0	843	US-09-314-701-47	Sequence 47, Appl
4	598.6	71.3	852	US-09-314-701-3	Sequence 3, Appl
5	243.4	29.0	849	US-09-648-520E-48	Sequence 48, Appl
6	238.4	28.4	924	US-09-314-701-35	Sequence 35, Appl
7	238.4	28.4	1607	US-09-660-587-1	Sequence 1, Appl
8	238.4	28.4	1607	US-09-261-358A-1	Sequence 1, Appl
9	238.4	28.4	1607	US-09-648-520E-47	Sequence 47, Appl
10	238.4	28.4	1607	US-09-201-458-1	Sequence 1, Appl
11	238.4	28.4	1607	US-09-811-007A-1	Sequence 1, Appl
12	234	27.9	840	US-09-660-587-5	Sequence 5, Appl
13	234	27.9	840	US-09-261-358A-5	Sequence 5, Appl
14	234	27.9	840	US-09-811-007A-5	Sequence 5, Appl
15	232.4	27.7	846	US-09-314-701-37	Sequence 37, Appl
16	232.4	27.7	846	US-09-314-701-1	Sequence 1, Appl
17	228.6	27.2	830	US-08-953-326-11	Sequence 11, Appl
18	228.6	27.2	830	US-09-553-662-11	Sequence 11, Appl
19	228.6	27.2	830	US-10-062-994-11	Sequence 11, Appl
20	217.4	25.9	867	US-09-314-701-31	Sequence 31, Appl
21	212.8	25.3	861	US-08-953-326-8	Sequence 8, Appl
22	212.8	25.3	861	US-09-314-701-7	Sequence 7, Appl
23	212.8	25.3	861	US-09-553-662-8	Sequence 8, Appl
24	212.8	25.3	861	US-10-062-994-8	Sequence 8, Appl
25	207.2	24.7	843	US-08-953-326-10	Sequence 10, Appl
26	207.2	24.7	843	US-09-314-701-11	Sequence 11, Appl
27	207.2	24.7	843	US-09-553-662-10	Sequence 10, Appl

28	207.2	24.7	843	4	US-10-062-994-10	Sequence 10, Appl
29	205	24.4	837	3	US-08-953-326-9	Sequence 9, Appl
30	205	24.4	837	4	US-09-314-701-9	Sequence 9, Appl
31	205	24.4	837	4	US-09-553-662-9	Sequence 9, Appl
32	205	24.4	837	4	US-10-062-994-9	Sequence 9, Appl
33	203.8	24.3	842	3	US-08-733-230-3	Sequence 3, Appl
34	203.8	24.3	842	3	US-08-953-326-3	Sequence 3, Appl
35	203.8	24.3	842	3	US-09-553-662-3	Sequence 3, Appl
36	203.8	24.3	842	4	US-10-062-994-3	Sequence 3, Appl
37	198.4	23.6	843	4	US-09-314-701-5	Sequence 5, Appl
38	195	23.2	828	3	US-09-660-587-43	Sequence 43, Appl
39	195	23.2	828	4	US-09-811-007A-43	Sequence 43, Appl
40	195	23.2	864	3	US-08-733-230-1	Sequence 1, Appl
41	195	23.2	864	3	US-08-953-326-1	Sequence 1, Appl
42	195	23.2	864	4	US-09-553-662-1	Sequence 1, Appl
43	195	23.2	864	4	US-10-062-994-1	Sequence 1, Appl
44	191.8	22.8	831	4	US-09-314-701-41	Sequence 41, Appl
45	185.4	22.1	840	4	US-09-314-701-23	Sequence 23, Appl

ALIGNMENTS

```

RESULT 1
US-09-660-587-41
; Sequence 41, Application US/09660587
; Patent No. 6392023
; GENERAL INFORMATION:
; APPLICANT: Walker, David H.
; APPLICANT: McBride, Jere W.
; APPLICANT: Yu, Xue-Jie
; TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
; FILE REFERENCE: D6152CP2
; CURRENT APPLICATION NUMBER: US/09/660,587
; PRIORITY FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/261,358
; PRIORITY FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 41
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: nucleic acid sequence of E. canis p28-2
US-09-660-587-41

Query Match      100.0%; Score 840; DB 3; Length 840;
Best Local Similarity 100.0%; Pred. No. 1.1e-211;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGAATTATAGAAATTTCTAGTAGAAGCGCTTATCTCATTAATGTAATCTTACCA 60
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DB      1 ATGAATTATAGAAATTTCTAGTAGAAGCGCTTATCTCATTAATGTAATCTTACCA 60

QY      61 TATAGCTTTTGGAGATCTCTGAGTTCAAGAACTATATGTAATCAAGAAAGCTTAC 120
        |||
DB      61 TATAGCTTTTGGAGATCTCTGAGTTCAAGAACTATATGTAATCAAGAAAGCTTAC 120

QY      121 ATTAGTCAAGTACCAATTCACATTAATCACTTTAGAAATTTCTGCTGAAGAACT 180
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QY      181 CCTATTATAGGAACAATTTCTTCACTAAAGTTTTCGACCTAAAGAAAGTGGAT 240
        |||
DB      181 CCTATTATAGGAACAATTTCTTCACTAAAGTTTTCGACCTAAAGAAAGTGGAT 240

QY      241 ATTAACAAAAAGAGATTTTACAGAGTAGCTCCAGCAATTTTCAAAATTACTTA 300
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DB      241 ATTAACAAAAAGAGATTTTACAGAGTAGCTCCAGCAATTTTCAAAATTACTTA 300

QY      301 ATATACAGATTTTCAAGAGTATTTGTTACTCTATAGACGACCAAGATTAAGACTTGA 360
        |||
DB      301 ATATACAGATTTTCAAGAGTATTTGTTACTCTATAGACGACCAAGATTAAGACTTGA 360

```

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OM nucleic - nucleic search, using bw model

Run on: February 19, 2005, 18:37:19 ; Search time 3559 Seconds
(without alignments)
8983.980 Million cell updates/sec

Title: US-10-680-349-41

Perfect score: 840
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Scoring table: IDENTITY NUC
Gapop 10%0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1.*
2: gb_est2.*
3: gb_hc1.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsa1.*
9: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68.6	8.2	1101	9	CNS00EVL AL069706 Drosophila
2	63.4	7.5	750	9	CNS011ID AL100303 Drosophila
3	59.2	7.0	895	8	AZ550258 ENTFU14TF
4	58.2	6.9	875	8	AZ550139 AZ550139
5	56.8	6.8	927	8	AZ549396 ENTE86TR
6	56.8	6.8	937	8	BH155225 ENTFM38TF
7	55.8	6.6	889	8	AZ547516 ENTFM38TF
8	55.8	6.6	1101	9	CNS0039G AL063921 Drosophila
9	55	6.5	627	5	BQ475055 carabuid
10	55	6.5	770	5	BQ474983 BQ474983
11	55	6.5	1101	9	CNS0039G AL063921 Drosophila
12	54.8	6.5	1348	9	CG749499 P043-4-A0
13	54.2	6.5	939	9	CNS0170D AL108367 Drosophila
14	54.2	6.5	939	8	BH133767 ENTFU23TF
15	53.6	6.4	897	8	AZ551013 AZ551013
16	53	6.3	1101	9	CNS0176 AL108540 Drosophila
17	52.8	6.3	895	8	BH163498 ENTFU07TR
18	52.8	6.3	922	8	BH136172 ENTFU07TR
19	52.4	6.2	984	9	CL113045 ISB1-57P1
20	52.4	6.2	1487	9	ACG390845 Mus muscu
21	52	6.2	841	8	AZ689408 ENTFU95TR
22	51.8	6.2	884	8	CNS0129A AL101272 Drosophila
23	51.6	6.1	606	4	B1441163 B1441163
24	51.6	6.1	819	8	AZ677439 ENTFU69TF

C 25	51.6	6.1	833	8	AZ544101	AZ544101 ENTFP80TF
C 26	51.6	6.1	912	8	AZ545164	AZ545164 ENTFW83TR
C 27	51.6	6.1	912	8	BH158221	ENTSD60TF
C 28	51.6	6.1	917	8	BH166533	ENTSU42TF
C 29	51.6	6.1	928	8	BH164168	ENTSD24TR
C 30	51.4	6.1	878	9	CNS0187R	AL108991 Drosophila
C 31	51.2	6.1	884	8	AZ689586	ENTHU07TR
C 32	51	6.1	898	8	AZ538693	AZ538693 ENTFG73TF
C 33	51	6.1	932	8	BH132524	BH132524 ENTFM36TF
C 34	50.8	6.0	1001	9	CNS0155H	AL105023 Drosophila
C 35	50.6	6.0	747	9	CNS011RO	AL100640 Drosophila
C 36	50.6	6.0	1013	9	AG564361	AG564361 Mus muscu
C 37	50.6	6.0	1224	9	AG305050	AG305050 Mus muscu
C 38	50.4	6.0	649	4	BH160056	BH160056 ESTS62579
C 39	50.4	6.0	852	8	AZ529741	AZ529741 ENTFCA0TR
C 40	50.2	6.0	1201	9	AG390499	AG390499 Mus muscu
C 41	50	6.0	481	4	B133673	B133673 k166a05.Y
C 42	50	6.0	762	9	AG524600	AG524600 Mus muscu
C 43	50	6.0	885	8	BH167558	BH167558 ENTFZ50TR
C 44	50	6.0	886	8	BH146655	BH146655 ENTFE52TF
C 45	50	6.0	908	8	BH152307	BH152307 ENTFV06TR

ALIGNMENTS

RESULT 1
LOCUS CNS00EVL 1101 bp DNA linear GSS 04-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RFL1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL069706 GI:4949849
VERSION AL069706
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Oosawa and Aaron Mammola in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RFL1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
1. 1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29B23"
/clone_id="RFL1-98"
/note="end : T7"
ORIGIN
Query Match 8.2%; Score 68.6; DB 9; Length 1101;
Best Local Similarity 34.7%; Pred. NO. 1.5e-05;

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OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 17:06:08 ; Search time 4113 Seconds

(without alignments)
9896.032 Million cell updates/sec

Title: US-10-680-349-41

Perfect score: 840

Sequence: 1 atgaatataagaataatct.....ttggaatgaggtcacccttc 840

Scoring table: IDENTITY NUC

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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3: gb_in:*
4: gb_om:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sbs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	840	100.0	AR437334	Sequence
2	840	100.0	AR303107	Sequence
3	840	100.0	AF528511	Ehrlichia
4	840	100.0	AF528512	Ehrlichia
5	840	100.0	AF528514	Ehrlichia
6	840	100.0	AF528515	Ehrlichia
7	840	100.0	AF528515	Ehrlichia
8	840	100.0	AF528515	Ehrlichia
9	840	100.0	AF528515	Ehrlichia
10	840	100.0	AF528515	Ehrlichia
11	840	100.0	AF528515	Ehrlichia
12	840	100.0	AF528515	Ehrlichia
13	840	100.0	AF528515	Ehrlichia
14	840	100.0	AF528515	Ehrlichia
15	840	100.0	AF528515	Ehrlichia
16	840	100.0	AF528515	Ehrlichia
17	840	100.0	AF528515	Ehrlichia
18	840	100.0	AF528515	Ehrlichia
19	840	100.0	AF528515	Ehrlichia

20	598.6	71.3	852	6	AR303085	Sequence
21	528.2	62.9	3507	1	AF125276	Cowdria r
22	528.2	62.9	3535	1	AF125277	Cowdria r
23	528.2	62.9	3538	1	AF125277	Cowdria r
24	528.2	62.9	3541	1	AF125279	Cowdria r
25	528.2	62.9	3551	1	AF125275	Cowdria r
26	528.2	62.9	3572	1	AF125278	Cowdria r
27	528.2	62.9	24993	1	AY343331	Cowdria r
28	457.6	54.5	2362	1	AF319940	Cowdria r
29	238.4	28.4	834	1	AF082745	Ehrlichia
30	238.4	28.4	834	1	AF082746	Ehrlichia
31	238.4	28.4	834	1	AF082747	Ehrlichia
32	238.4	28.4	834	1	AF082748	Ehrlichia
33	238.4	28.4	834	1	AF082749	Ehrlichia
34	238.4	28.4	834	1	AF082750	Ehrlichia
35	238.4	28.4	924	6	AR303101	Sequence
36	238.4	28.4	1607	6	AR213516	Sequence
37	238.4	28.4	1607	6	AR235244	Sequence
38	238.4	28.4	1607	6	AR437310	Sequence
39	234	27.9	840	6	AR213518	Sequence
40	234	27.9	840	6	AR437312	Sequence
41	234	27.9	1050	1	AY117396	Ehrlichia
42	234	27.9	1342	1	AF393388	Ehrlichia
43	233.2	27.8	1315	1	AF393392	Ehrlichia
44	232.4	27.7	843	6	AR303102	Sequence
45	232.4	27.7	846	6	AR303084	Sequence

ALIGNMENTS

RESULT 1	AR437334	840 bp	DNA	linear	PAT 18-DEC-2003
LOCUS	AR437334	Sequence 41 from patent US 660269.			
DEFINITION	AR437334				
ACCESSION	AR437334.1	GI:40202246			
VERSION	AR437334.1	GI:40202246			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 840)				
AUTHORS	Walker, D.H., Yu, X.-J. and McBride, J.W.				
TITLE	Homologous 28-kilodalton immunodominant protein genes of Ehrlichia				
JOURNAL	Patent: US 660269-A 41 09-DEC-2003;				
FEATURES	Location/Qualifiers				
source	1..840				
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	/mol_type="genomic DNA"				
Query Match	100.0%; Score 840; DB 6; Length 840;				
Best Local Similarity	100.0%; Pred. No. 3, ie-140;				
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Db	1 ATGAATTATTAAGAAATTCCTAGTAAGAGCGGTTAATTCATTATGTCATCTTACCA 60				
Qy	61 TATCAGCTTTTGGAGATCCTGTAAGTCAAGAACTAATATCAAGAAAGGCTTAC 120				
Db	61 TATCAGCTTTTGGAGATCCTGTAAGTCAAGAACTAATATCAAGAAAGGCTTAC 120				
Qy	121 ATTGTCGAAGTCAATCAAGTATATCACTTGAAGAAATTCCTGCTGAAGAACT 180				
Db	121 ATTGTCGAAGTCAATCAAGTATATCACTTGAAGAAATTCCTGCTGAAGAACT 180				
Qy	181 CCTATTAATGGAACAAATTCCTCACTTAAGAAAGTATGATGAT 240				
Db	181 CCTATTAATGGAACAAATTCCTCACTTAAGAAAGTATGATGAT 240				
Qy	241 ATTAACAAAAAGACGATTTTACAGAGTGCACGACATGATTTTCAAAATACCTA 300				

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 DB 61 PINGNSLTGKVFGLKKGDDITKKDDPTRVAPGIDPQNNLISGFSGSIYSGMDGRIELE 120
 QY 121 AAYQFNPKNNTDNDTNGEYKGFALSRKDAEDQYVVLKNDGITFMSLMVNTCYDIT 180
 DB 121 AAYQFNPKNNTDNDTNGEYKGFALSRKDAEDQYVVLKNDGITFMSLMVNTCYDIT 180
 QY 181 AEGVSFVPYACAGIGADLITTFKDLNLKFAVQKIGISYPTPEVSAGFIQYHYGVGNK 240
 DB 181 AEGVSFVPYACAGIGADLITTFKDLNLKFAVQKIGISYPTPEVSAGFIQYHYGVGNK 240
 QY 241 FEKIPVITPVVNDAPQTTASVTLVGVFGSEIGKRFTE 280
 DB 241 FEKIPVITPVVNDAPQTTASVTLVGVFGSEIGKRFTE 280

RESULT 2

ABG7958
 ID ABG7958 standard; protein; 280 AA.

AC ABG7958;

DT 15-NOV-2002 (first entry)

DE Ehrlichia canis outer membrane protein (P30F) #9.

KW Outer membrane protein; OMP; P30F; ehrlichiosis; infection.

OS Ehrlichia canis.

XX US200220115-A1.

PD 29-AUG-2002.

PF 28-JAN-2002; 2002US-00059964.

PR 19-MAY-1999; 99US-00314701.

PA (RIKI/) RIKIHISA Y.

PI (OHAS/) OHASHI N.

PI Rikihisa Y, Ohashi N;

XX WPI; 2002-618954/66.

DR N-PSDB; ABS63299.

XX Isolated polynucleotide encoding an outer membrane protein of E. canis or

PT B. chaffeensis used in the diagnosis of infection.

PS Claim 10; Fig 30B; 49pp; English.

XX The invention relates to an isolated polynucleotide encoding an outer
 CC membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis used
 CC in the diagnosis of infection. An infection such as human ehrlichiosis or
 CC canine ehrlichiosis can be diagnosed by providing a serum sample from the
 CC patient, providing a polypeptide or mixture of polypeptides, contacting
 CC the sample with the polypeptide and assaying for the formation of a
 CC complex between antibodies in the serum sample and the polypeptide, where
 CC formation of a complex is indicative of infection with E. chaffeensis.
 CC This sequence represents an Ehrlichia outer membrane protein of the
 CC invention

XX Sequence 280 AA;

Query Match 100.0%; Score 1462; DB 5; Length 280;
 Best Local Similarity 100.0%; Pred. No. 1.9e-138;
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 121 AAYQFNPKNNTDNDTNGEYKGFALSRKDAEDQYVVLKNDGITFMSLMVNTCYDIT 180
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 DB 181 AEGVSFVPYACAGIGADLITTFKDLNLKFAVQKIGISYPTPEVSAGFIQYHYGVGNK 240
 QY 241 FEKIPVITPVVNDAPQTTASVTLVGVFGSEIGKRFTE 280
 DB 241 FEKIPVITPVVNDAPQTTASVTLVGVFGSEIGKRFTE 280

RESULT 3

ADA09781
 ID ADA09781 standard; protein; 280 AA.

AC ADA09781;

DT 06-NOV-2003 (first entry)

DE E. canis outer membrane protein P30-10.

KW outer membrane protein; circulating leukocyte; monocytic ehrlichiosis;
 KW Rocky Mountain spotted fever; canine ehrlichiosis; antigen.

OS Ehrlichia canis.

XX US644517-B1.

PN 08-APR-2003.

PF 19-MAY-1999; 99US-00314701.

PR 18-SEP-1998; 98US-0100843P.

PA (OHIS) UNIV OHIO STATE RES FOUND.

PI Rikihisa Y, Ohashi N;

XX WPI; 2003-553952/52.

DR N-PSDB; ADA09780.

XX New isolated polynucleotide encoding outer membrane protein p30 of
 PT Ehrlichia canis or its variant or fragment, useful for producing
 PT Ehrlichia canis or Ehrlichia chaffeensis outer membrane proteins for
 XX diagnosing and treating ehrlichiosis.

PS Disclosure; Fig 30; 105pp; English.

XX The invention relates to an isolated polynucleotide encoding a variant of
 CC the outer membrane protein (OMP) P30 of Ehrlichia canis, an outer
 CC membrane protein of E. canis, or an antigenic fragment of the E. canis
 CC P30 protein, or comprising a sequence which is the complement of
 CC nucleotide 99 through nucleotide 672 of ADA09764. Also disclosed are E.
 CC canis and E. chaffeensis outer membrane proteins and their encoding
 CC nucleic acids. The polynucleotides are useful for producing E. canis or
 CC E. chaffeensis outer membrane protein, for designing hybridisation probes
 CC or its allelic forms, for designing primers for PCR. The polypeptides
 CC encoded by the polynucleotide is useful for diagnosing human ehrlichiosis
 CC (Rocky mountain spotted fever) or canine ehrlichiosis. The present
 CC sequence represents an E. canis outer membrane protein.

XX Sequence 280 AA;

Query Match 100.0%; Score 1462; DB 6; Length 280;
 Best Local Similarity 100.0%; Pred. No. 1.9e-138;
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MMYKILVRSALISLMSILPYQSPADPVGSR---TNDKKEGYISAKNPSISHRKPSA 60
DB 1 MMYKILVRSALISLMSILPYQSPADPVGSR---TNDKKEGYISAKNPSISHRKPSA 60
QY 61 PINGNSLTKKVFGLKKGDDITFKODFTVAPEIDFQNNLISGFSGISYMDGPRIE 120
DB 61 PINGNSLTKKVFGLKKGDDITFKODFTVAPEIDFQNNLISGFSGISYMDGPRIE 120
QY 121 AAYQGFNPKNNTDNDTNGEYKHFALSRKDMEDQYVVLKNDGITFMSLWNTCYDT 180
DB 121 AAYQGFNPKNNTDNDTNGEYKHFALSRKDMEDQYVVLKNDGITFMSLWNTCYDT 180
QY 181 AAGVSVFPYACAGIGADLITTFKDLMLKFAVGKIGISYPTPEVSAPFGYHGVY 240
DB 181 AAGVSVFPYACAGIGADLITTFKDLMLKFAVGKIGISYPTPEVSAPFGYHGVY 240
QY 241 FEKIPVITPVVNDAPQTTSASVTLVDVGFGEIGMRTF 280
DB 241 FEKIPVITPVVNDAPQTTSASVTLVDVGFGEIGMRTF 280

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RESULT 4
 ID AAY06944 standard; protein; 283 AA.

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XX AC AAY06944;
XX DT 27-AUG-2003 (revised)
XX DT 05-JUL-1999 (first entry)
XX DB E. chaffeensis OMP-1B protein.
XX KW Outer membrane protein; OMP; Ehrlichia chaffeensis; E. canis; P30;
XX KW detection; dog.
XX OS Ehrlichia chaffeensis.
XX PN W09913720-A1.
XX PD 25-MAR-1999.
XX PF 18-SEP-1998; 98WO-US019600.
XX PR 19-SEP-1997; 97US-0059353P.
XX PA (OHIS ) UNIV OHIO STATE.
XX PI Rikihisa Y, Ohashi N;
XX DR WPI; 1999-254290/21.
XX DR N-PSDB; AAX34744.
XX PT Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia
XX PT canis.
XX PS Claim 12; Fig 4B; 55pp; English.
XX CC The invention provides isolated outer membrane proteins (OMP) from
XX CC Ehrlichia chaffeensis and E. canis. The E. chaffeensis proteins form part
XX CC of the OMP family and consist of proteins OMP-1, -11B to Z) shown in
XX CC AAY06943-958. The E. canis proteins form part of the P30 family and
XX CC consist of proteins shown in AAY06959-970. The proteins and genes are
XX CC used to detect E. chaffeensis in patients and E. canis in dogs. (Updated
XX CC on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 283 AA;

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Query Match 82.3%; Score 1202.5; DB 2; Length 283;

Best Local Similarity 79.5%; Pred. No. 2.6e-112;
 Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;

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QY 1 MMYKILVRSALISLMSILPYQSPADPVGSR---TNDKKEGYISAKNPSISHRKPSA 57
DB 1 MMYKILVRSALISLMSILPYQSPADPVGSR---TNDKKEGYISAKNPSISHRKPSA 57
QY 58 EETPINGNSLTKKVFGLKKGDDITFKODFTVAPEIDFQNNLISGFSGISYMDGPRI 117
DB 61 EETPINGNSLTKKVFGLKKGDDITFKODFTVAPEIDFQNNLISGFSGISYMDGPRI 120
QY 118 EIEAAYQGFNPKNNTDNDTNGEYKHFALSRKDMEDQYVVLKNDGITFMSLWNTCY 177
DB 121 EIEAAYQGFNPKNNTDNDTNGEYKHFALSRKDMEDQYVVLKNDGITFMSLWNTCY 180
QY 178 DITAGSVFPYACAGIGADLITTFKDLMLKFAVGKIGISYPTPEVSAPFGYHGVY 237
DB 181 DITAGSVFPYACAGIGADLITTFKDLMLKFAVGKIGISYPTPEVSAPFGYHGVY 240
QY 238 GNFPEKIPVITPVVNDAPQTTSASVTLVDVGFGEIGMRTF 280
DB 241 GNFPEKIPVITPVVNDAPQTTSASVTLVDVGFGEIGMRTF 283

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RESULT 5
 ID AAU96106 standard; protein; 283 AA.

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XX AC AAU96106;
XX DT 07-AUG-2003 (revised)
XX DT 02-JUL-2002 (first entry)
XX DB Ehrlichia chaffeensis OMP-1B.
XX KW Ehrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial.
XX KW Ehrlichia chaffeensis.
XX OS Ehrlichia chaffeensis.
XX PN W0200222782-A2.
XX PD 21-MAR-2002.
XX PF 12-SEP-2001; 2001WO-US028759.
XX PR 12-SEP-2000; 2000US-00660587.
XX PA (RERE-) RES DEV FOUND.
XX PI Walker DH, Yu X, McBride JW;
XX DR WPI; 2002-351882/38.
XX PT New recombinant homologous 28 kilodalton immunodominant protein from
XX PT Ehrlichia canis, useful for treating Ehrlichia canis infections.
XX PS Example 3; Fig 3; 106pp; English.
XX CC The invention relates to a recombinant homologous 28 kDa immunodominant
XX CC protein, p28, (I), of Ehrlichia canis. (I), a 28-kDa antigen preferably
XX CC dispersed in a pharmaceutically acceptable carrier, is useful for
XX CC inhibiting E. canis infection in a subject. (I) is useful in the
XX CC development of vaccines and serodiagnostic tests that are particularly
XX CC effective for disease prevention and serodiagnosis. AAU96100-AAU96118
XX CC represent the 28-kDa antigen amino acid sequences of the invention.
XX CC (Updated on 07-AUG-2003 to correct OS field.)
XX SQ Sequence 283 AA;

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Query Match 82.3%; Score 1202.5; DB 5; Length 283;
 Best Local Similarity 79.5%; Pred. No. 2.6e-112;
 Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;